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DNA barcoding is a technique in which species identification is performed using DNA sequences from a small fragment of the genome, with the aim of contributing to a wide range of ecological and conservation studies in which traditional taxonomic identification is not practical. DNA barcoding is well established in animals using the cox1 gene (COI), but there is not yet any proposed universal barcode for plants that has received a broad consensus. We undertook intensive field collections in the renowned Kruger National Park (South Africa), which has its most southern part included in the Maputaland Biodiversity hotspot. Using a selection of trees and shrubs, we compared height potential barcodes: six advised by the plant working group and two from Kress et al. (2007). We applied a battery of metrics to measure intra- and inter-specific genetic divergences, statistical tests, phylogenetic and coalescence analyses. Compared to previous plant studies, we assessed to which extend a 'DNA barcoding gap' is present between intra- and inter-specific variations using multiple accessions per species. We identified a portion of the plastid matK gene as a universal DNA barcodes for flowering plants, which can be used singly or in combination with the trnH-psbA inter-gene for a slight increase in performance. Furthermore, we assessed the accuracy of combining to the previous barcode one of the two newly proposed loci by Ki-Joong Kim (University of Seoul). We further discuss the role that DNA barcoding can play in biodiversity inventories for conservation.

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A synchronous colonization of Madagascar by plants?

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Madagascar is renowned for the uniqueness of its fauna and flora with a high endemism. Because Madagascar separated from Africa and India before the diversification of angiosperms, its plant biodiversity is firstly due to colonization events across oceans followed by endemic radiations rather than vicariance. Although the literature can show a tendency in an asynchronous colonization of Madagascar by plants, it is not accurate to rely on such studies because of discrepancies in molecular dating techniques. Here we assess a possible synchronization in plant colonization of Madagascar from Africa by comparing the historical biogeography of 13 groups of plants showing Malagasy endemicity. Representatives from each group are included in a large *rbcL* matrix of 1566 taxa from which phylogenetic trees were inferred using PaupRat. One of the most parsimonious trees was dated by 23 calibrations points using three different dating methods, i.e. PL, NPRS, and a modified version by Ziheng Yang of the source of PAML for using MULTIDIVTIME. The results of this study provide crucial insight into trans-oceanic dispersal mechanism and the factors triggering radiation processes.

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Determining pathogen resistance in Arabidopsis by investigating the interaction between glutathione and non-xpressor of pathogenecity genes (NPR1)

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Reactive oxygen species (ROS) control many different processes in plants such as programmed cell death, pathogen defense and systemic signalling thus the steady state level of ROS in cells has to be tightly regulated as accumulation of ROS can be detrimental to the cell. This can be achieved in various ways such as antioxidants, ROS-scavenging enzymes, defense gene expression to name but a few. A key component of the antioxidant process is the thiol glutathione pathway catalysed by the enzyme glutathione reductase and glutathione synthetase. Glutathione has been associated with determining the redox state of the cell and may indirectly activate regulatory proteins such as non-expressor of pathogenicity genes (NPR1) which has been shown to play an important role in the induction of systemic acquired resistance. To date, no direct link has been established between glutathione and the NPR1 therefore the aim of my study is to investigate the interaction between glutathione and the NPR1 gene and what effect they have on pathogen resistance needs to be studied further.

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Colophospermum mopane wood utilisation in the Lowveld, Limpopo Province

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The wood and non-wood products from mopane woodland were quantified from six villages in the Lowveld, Limpopo Province, South Africa. One hundred and eighty individuals were interviewed from the selected villages. Three villages were located in the depleted woodlands and the remaining three at abundant woodlands. Traditional governance structures within the selected villages and relevant conservation department officials were also interviewed. *Colophospermum mopane* is an essential source of fuelwood and provide poles used for construction of traditional structures. Each family uses 6.8±0.1 kg of *C. mopane* fuelwood for cooking/day in the woodland depleted villages, while 8.2±0.2 kg is used at the woodland abundant villages. The average volume of wood consumed to construct an adult's hut is 0.24 m^3 in the woodland depleted villages and 0.33 m^3 in the woodland abundant villages. The role played by mopane worms to the wellbeing of the rural people was also assessed and options to promote efficient use of woodland resources were suggested.

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Clarification of generic delimitation in *Justicia* and *Siphonoglossa* (Acanthaceae)

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